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CDS
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/db_xref="SWISS-PROT:069415"
/translation="MFDIGFSELLLVFIIGLVVLGPQRLPVAVKTVAGWIRALRSLAT
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AAPSPSSSDKP"
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/citation=[1]
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847..1623
/gene="tatC"
CDS
847..1623
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LFMAFGVSFEVPPVAIVLLCWMGITSPEDLRKKRPyVLGAFVVGMLLTPPDVFSQTL
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1653..2447
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CDS
1653..2447
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TREEMQACVAHGIYIGITGWVCDERRGELRELLPLIPAEKLLIETDAPYLLPRDLTP
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 121 caaaaagctc ggctccatcg gttccgatct tggtgctcg atcaaaggct ttaaaaaaagc
 181 aatgagcgat gatgaaccaa agcaggataa aaccagtca gatgctgatt ttactgcgaa
 241 aactatcgcc gataagcagg cggatacgaa tcaggaacag gctaaaacag aagacgcgaa
 301 gcgccacgat aaagagcagg ttaatccgt gttgatatac gtttttagcg aactgctatt
 361 ggtgttcatc atcggcctcg tcgttctggg gccgcaacga ctgcctgtgg cggtaaaaac
 421 ggtagcgggc tggattcgcg cgttgcgttc actggcaca acggtgca gacgaaactgac
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 961 aatgacatct atcacctggt atccgcgcca ttgatcaagc agttgcgcgca aggttcaacg
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 1501 gcatcccgat tttactgtt gtttggaaatc ggtgttttct ttcacggtt ttacggttgg
 1561 aaaggcgaa atcgggaaga gggaaaacgac gctgaagcag aagcgaaaa aactgaagaa
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 1861 gcaagctcg gcaagctcg actgaagaag cgattattga gctggccgcg cagccagaag
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 1981 aggaacgcgc ttttggcc cagctacgc ttggccgaga tttaaacatg cggatttt
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 2401 ccaccacggaa tgctaatgtc aaaacactgt ttggattgc gtttttagagt ttgcggaa

//

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May 20 2003 11:20:12

have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the *E. coli* Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the *E. coli* Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The *E. coli* K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

FEATURES	Location/Qualifiers
<u>source</u>	1..11057 /organism="Escherichia coli K12" /mol_type="genomic DNA" /strain="K12" /sub_strain="MG1655" /db_xref="taxon:83333"
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<u>promoter</u>	27..56 /note="factor Sigma70; predicted +1 start at 4013913"
<u>gene</u>	168..929 /gene="udp" /note="synonym: b3831"
<u>CDS</u>	168..929 /gene="udp" /EC_number="2.4.2.3" /function="enzyme; Salvage of nucleosides and nucleotides" /note="o253; 100 pct identical to UDP_ECOLI SW: P12758" /codon_start=1 /transl_table=11 /product="uridine phosphorylase" /protein_id="AAC76834.1" /db_xref="GI:1790265" /translation="MSKSDVFHLGLTKNDLQGATLAIVGDPDRVEKIAALMDKPVKL ASHREFTTWRAELDGKPVIVCSTGIGGPSTSIAVEELAQLGIRTFLRIGTTGAIQPHI NVGDVLVTTASVRLDGASLHFAPLEFPAPADFECTTALVEAAKSIGATHVGVTASSD TFYPGQERYDTYSGRVRHFKGSMEEQAMGVMNYEMESATLLTMCASQGLRAGMVAG VIVNRQQEIPNAETMKQTESHAVKIVVEAARRLL"
<u>promoter</u>	1009..1037 /note="factor Sigma70; predicted +1 start at 4014894"
<u>gene</u>	1070..2497 /gene="yign" /note="synonym: b3832"
<u>CDS</u>	1070..2497 /gene="yign" /function="phenotype; Not classified" /note="o475; 99 pct identical amino acid sequence and equal length to YIGN_ECOLI SW: P27850" /codon_start=1 /transl_table=11

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GKEAQERHTLTHERNLQQLNAQMAQEAINLTRLAKGDNKTOQGNWGEVVLTRVLEASG
LREGYELYETQVSIENDARSRMQPDVIVRLPQGKDVVIDAKMTLVAYERYFNAEDDYTR
ESALQEHIASVRNHIRLLGRKDYQQLPGLRTLDYVLMFIPVEPAFLALDRQPELITE
ALKNNIMLVSPTTLLVALRTIANLWRYEHQSRNAQQIADRASKLYDKMRLFIDDMSAI
GQSLDKAQDNYRQAMKKLSSGRGNVLAQAEAFRGLGVEIKREINPDLAEQAVSQDEEY
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promoter


2451..2482
/gene="yigN"
/note="factor Sigma70; predicted +1 start at 4016339"


gene


2592..3347
/gene="ubiE"
/note="synonym: b3833"


CDS


2592..3347
/gene="ubiE"
/function="enzyme; Biosynthesis of cofactors, carriers:
Menaquinone, ubiquinone"
/note="o251; 100 pct identical to YIGO_ECOLI SW: P27851"
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/product="2-octaprenyl-6-methoxy-1,4-benzoquinone -->
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FGIHRLWKRTIDCSGVRGGQTVLDLAGGTGDLTAKFSRLVGETGKVVLADINESMPK
MGREKLRNIGVIGNVEYVQANAEALPPFDNTFDCITISFGLRNVTDKDALKRSMYRVL
KPGGRLLVLEFSKPIIEPLSKAYDAYSFHVLPRIGSLVANDADSYRYLAESIRMHPDQ
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gene


3361..3966
/gene="yigP"
/note="synonym: b3834"


CDS


3361..3966
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P27852) but the N- andC-terminal sequences are unaltered"
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/db_xref="GI:2367308"
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STSLILVFSERQVDVLGEWADACTVIAYASVLPKLRDRQQLTALIRSGELEVQGDI
QVQNFVALADLAEFDPAELLAPYTGDIAAEGISKAMRGGAFLHHGIKRQQRYVAEA
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promoter


3858..3875
/gene="yigP"
/note="factor Sigma54; predicted +1 start at 4017732"


gene


3963..5603
/gene="yigR"
/note="synonym: b3835"


CDS


3963..5603
/gene="yigR"
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/note="o546; sequence change joins ORFs yigQ, yigR, and
yigS from earlier version (YIGQ_ECOLI SW: P27853;
YIGR_ECOLI SW: P27854; YIGS_ECOLISW: P27855); very good
match to Azotobacter chroococcum partial ORF1 GB: U48404"
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PVIKADLKLIYRLARWVPRLLPDGRRRLPTEVVREYEKTLIDELNLLRESANAIQLRR
NFEDSPMLYIPEVVPDYCSEGMMVMERIYGIPVSDVAALEKNGTNMKLLAERGVQVFF
TQVFRDSFFFADMPGNIFVSYEHPPENPKYIGIDCGIVGSLNKEKDRLAENFIAFFN
RDYRKVAELHVDSGWVPPDTNVEEFEFAIRTVCPEIFEKPLAEISFGHVLLNLNFNTAR
RFNMEVQPQLVLLQKTLLYVEGVGRQLYPQLDLWKTAKPFLIESWIKDQVGIPALVRAF
KEKAPFWVEKMPPELPELVDLSLRQGKYLQHSDVKIARELQSNHVRQGQSRYFLGIGAT
LVLSGTFLVSRPEWGLMPGWLMAAGGLIAWFVGWRKTR"

gene 5640..5951
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CDS 5640..5951
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/codon_start=1
/transl_table=11
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/db_xref="GI:2367310"
/translation="MRLCLIIYHRGTCMGGISIWQLLIAVIVVLLFGTKKLGSIGS
DLGASIKGFKKAMSDDEPKQDKTSQDADFTAKTIADKQADTNQEQA
KTEDAKRHDKEQV"

gene 5815..6156
/gene="b3837"
CDS 5815..6156
/gene="b3837"
/function="putative factor; Not classified"
/note="o113; sequence change split ORF of earlier
version; was part of yigT (o261; YIGT_ECOLI SW: P27856)"
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/transl_table=11
/product="putative histone"
/protein_id="AAC76840.1"
/db_xref="GI:2367311"
/translation="MMNQSRIKPVRMLILLRKLSPISSRRIRIRNRLKQKTRSATIKSR
CNPCLISVLANCYWCSSSASPPSGAATTACGGKNGSGLDSRVAFTGDNGAERTDPGVK
TPGVSGQSEKG"

gene 6035..6472
/gene="b3838"
CDS 6035..6472
/gene="b3838"
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/note="o145; sequence change split ORF of earlier
version; was part of yigT (o261; YIGT_ECOLI SW: P27856)"
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6475..7251
/gene="yigU"
/note="synonym: b3839"
CDS
6475..7251
/gene="yigU"
/function="orf; Unknown"
/note="o258; sequence change joins two ORFs relative
to earlier version; 97.7 pct identical to the conceptual
ORF YIGU_ECOLI SW: P27857"
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7281..7901
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/note="synonym: b3840"
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of a 264 aa conceptual translation YIGW_ECOLI SW: P27859"
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7735..8076
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/note="synonym: b3841"
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7735..8076
/gene="yigW_2"
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conceptual translation YIGW_ECOLI SW: P27859"
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gene
complement(8073..8561)
/gene="rfaH"
/note="synonym: b3842"

CDS
complement (8073..8561)
/gene="rfaH"
/function="regulator; Macromolecule metabolism:
Lipopolysaccharide"
/note="f162; 100 pct identical to RFAH_ECOLI SW: P26614;
alternate gene names sfrB, hlyT"
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of lipopolysaccharide core, F pilin, and haemolysin"
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DIVDPATPYPGDKVIITEGAFEGFQAIFFEPDGGEARSMLLNLINKEIKHSVKNTEFR
KL"
promoter
complement (8591..8619)
/note="factor Sigma70; predicted +1 start at 4022434"
8672..8704
promoter
/note="factor Sigma70; predicted +1 start at 4022561"
8728..10221
gene
/gene="yigC"
/note="synonym: b3843"
CDS
8728..10221
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/note="o497; ??? pct identical to conceptual
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AAHPGERFPVS
VALGADPATILGA
VTPV
PDTLSEYAFAGLLRGTKTEVVKCISNDLEV
PASAEIVLEGY
IEQGETAPEGPYGDHTGYYNEVDSFPVFTVTHITQREDAIYH
STYTGRPPDEPAVLGV
ALNEVFP
VPILOQKQFPEI
VDFYL
PPEGCSYR
LA
VTTIKKQYAGHAKR
VMMGVWSFLRQF
MYTKFVIV
CDDDV
NARD
WND
VI
WAIT
TRMDP
ARD
T
VL
VENT
P
IDY
LDF
ASP
V
SGL
GSK
MGL
DAT
NKWP
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QRE
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PIK
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IDAI
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ELA
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NNG
KSA"
gene
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CDS
10267..10968
/gene="ubiB"
/EC_number="1.6.8.-"
/function="enzyme; Energy metabolism, carbon: Electron
transport"
/note="o233; 99 pct identical amino acid sequence and
equal length to UBIB_ECOLI SW: P23486; similar to
monooxygenase subunits from *Methylococcus capsulatus* and
Pseudomonas putida"
/codon_start=1
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/product="ferrisiderophore reductase; flavin reductase
(NADPH:flavin oxidoreductase)"
/protein_id="AAC76847.1"
/db_xref="GI:2367314"

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 ERPMILIAAGGTGFSYARSILLTALARPNRNDITIYWGGREEQHLYDLCELEALSLKHP
 GLQVVPVVEQPEAGWRGRTGTVLAVLQDHGTLAEHDIYIAGRFE MAKIARDLFCSER
 NAREDRLFGDAFAFI"

BASE COUNT 2621 a 2682 c 3073 g 2681 t
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 61 gcaacgcatt tgcgtcatgg ttagtggat cacaaaaaaa tggtaaaccc ttcgttaaag
 121 tgcgtttttg cttcttctga ctaaaccgat tcacagagga gttgtatatg tccaaagtctg
 181 atgtttttca tctcgccctc actaaaaacg atttacaagg ggctacgcctt gccatcgctcc
 241 ctggcgaccc ggatcggtg gaaaagatcg ccgcgtat ggataagccg gttaaagctgg
 301 catctcaccg cgaattcact acctggcggtg cagagctgga tggtaaacct gttatcgct
 361 gctctaccgg tatacgccgc ccgtctaccc ttatgtgt tgaagagctg gcacagctgg
 421 gcattcgac cttcctcggt atcggtaaaa cgggcgtat tcagcccat attaatgtgg
 481 gtatgtcct ggttaccacg ggctctgtcc gtctggatgg cgcgagccg cacttcgcac
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May 20 2003 11:20:12



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Γ 1: AE000167. *Escherichia coli* ...[gi:1786836]

Links

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DEFINITION Escherichia coli K12 MG1655 section 57 of 400 of the complete genome.
ACCESSION AE000167 U00096
VERSION AE000167.1 GI:1786836
KEYWORDS .
SOURCE Escherichia coli K12
ORGANISM Escherichia coli K12
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 10264)
AUTHORS Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V., Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y.
TITLE The complete genome sequence of Escherichia coli K-12
JOURNAL Science 277 (5331), 1453-1474 (1997)
MEDLINE 97426617
PUBMED 9278503
REFERENCE 2 (bases 1 to 10264)
AUTHORS Blattner,F.R.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
REFERENCE 3 (bases 1 to 10264)
AUTHORS Blattner,F.R.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
REFERENCE 4 (bases 1 to 10264)
AUTHORS Plunkett,G. III.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
COMMENT This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG

Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

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